Please replace Table 2K on page 35 with the following:

Table 2K. Domain Analysis of NOV2
gnl|Smart|smart00110, C1Q, Complement component C1q domain.; Globular domain found in many collagens and eponymously in complement C1q. When part of full length proteins these domains form a 'bouquet' due to the multimerization of heterotrimers. The C1q fold is similar to that of tumour necrosis factor. CD-Length = 132 residues, 84.1% aligned Score = 86.7 bits (213), Expect = 1e-18

```
Query:  91   MAVTFDKVYVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLSVKLMKNRDEVQAMI
150
             V FDKV  N  G +D + G F C +PG Y+FS+ + +    + + V LMKN  +V
Sbjct:  20   QPVRFDKVLYNQQGHYDPSTGKFTCPVPGVYYFSYHI-ESKGRNVKVSLMKNGIQVMRE-   77

Query: 151   YDDGASRRREMQSQSVMLALRRGDAVWLLSHDHDGYGAYSNHGKYITFSGFLVY   204
             D+       ++ S   +L LR+GD VW L  D    G Y+        TFSGFL++
Sbjct:  78   CDEYQKGLYQVASGGALLQLRQGDQVW-LELDDKKNGLYAGEEVDSTFSGFLLF   130  (SEQ
ID NO: 182)
```

Please replace Table 3E on page 45 with the following:

Table 3E Domain Analysis of NOV3

gnl|Smart|smart00220, S_TKc, Serine/Threonine protein kinases, catalytic domain; Phosphotransferases. Serine or threonine-specific kinase subfamily.

CD-Length = 256 residues, 100.0% aligned
Score = 237 bits (605), Expect = 1e-63

```
Query:  191  FSVHRIIGRGGFGEVYGCRKRDTGKMYAMKCLDKKRIKMKQGETLALNERIMLSLVSTGD
        250
             + +   ++G+G FG+VY  R + TGK+ A+K + K+++K K+ E   L E  +L  +   D
Sbjct:  1    YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKLKKKKRER-ILREIKILKKL---D
        56

Query:  251  CPFIVCMSYAFHTPDKLSFILDLMNGGDLHYHLSQHGVFSEADMRFYAAEIILGLEHMHN
        310
             P IV +   F  DKL +++    GGDL  L + G  SE + RFYA +I+  LE++H+
Sbjct:  57   HPNIVKLYDVFEDDDKLYLVMEYCEGGDLFDLLKKRGRLSEDEARFYARQILSALEYLHS
        116

Query:  311  RFVVYRDLKPANILLDEHGHVRISDLGLACDFSKKKPHAS--VGTHGYMAPEVLQKGVAY
        368
             +  +++RDLKP NILLD  GHV+++D GLA        +    VGT  YMAPEVL  G Y
Sbjct:  117  QGIIHRDLKPENILLDSDGHVKLADFGLAKQLDSGGTLLTTFVGTPEYMAPEVL-LGKGY
        175

Query:  369  DSSADWFSLGCMLFKLLRGHSPFRQHKTKDK-HEIDRMTLTMAVELPDSFSPELHSLLEG
        427
             + D +SLG +L++LL G  PF          +                 SPE   L++
Sbjct:  176  GKAVDIWSLGVILYELLTGKPPFPGDDQLLALFKKIGKPPPPFPPPEWKISPEAKDLIKK
        235

Query:  428  LLQRDVNRRLGCLGRGAQEVKESPFF    453
             LL +D  +RL      A+E  E PFF
Sbjct:  236  LLVKDPEKRL-----TAEEALEHPFF    256 (SEQ ID NO: 183)
```

Please delete the paragraph following Table 3E on page 45.

Please replace Table 4E on page 63 with the following:

Table 4E. Domain Analysis of NOV4

gnl|Pfam|pfam01500, Keratin_B2, Keratin, high sulfur B2 protein. High sulfur proteins are cysteine-rich proteins synthesized during the differentiation of hair matrix cells, and form hair fibers in association with hair keratin intermediate filaments. This family has been divided up into four regions, with the second region containing 8 copies of a short repeat. This family is also known as B2 or KAP1.

CD-Length = 144 residues, 87.5% aligned
Score = 38.9 bits (89), Expect = 0.004

```
Query:  630  CIDVACSNHGTCITGTCICNPGYKGESCEEVDCMDPTCSGRGVCVRGECHCFVGWGGTNC
        689
             C   CS GTC +  C      +  SC +  C  P CS    C R C       + C
Sbjct:  5    CGFPTCSTLGTCGSSCC------QPPSCCQPSCCQPVCSQTTCC-RPTCFQSSCCRPSCC
        57


Query:  690  ETP--RATCLDQCSGHGTFLPDTGLCSCDPSWTGHDCSIEICAADCGGHGVCVGGTCRCE
        747
             +T  +  TC    S         G+ SC    W   DC +E
Sbjct:  58   QTSCCQPTCCQSSSCQ----TGCGIGSCRTRWCRPDCRVE-------------------
        93


Query:  748  DGWMGAACDQRACHPRCAEHGTCRDGKCECS---PGWNGEHC   786
             C   C   C    C+    + S  P + G+ C
Sbjct:  94   -.----GTCLPPCCVVSCTPPTCCQPVSAQASCCRPSYCGQSC   130  (SEQ ID NO:
        184)
```

Please replace Table 6G on pages 84-85 with the following:

Table 6G. Domain Analysis of NOV6

gnl|Pfam|pfam01404, EPH_lbd, Ephrin receptor ligand binding domain. The Eph receptors, which bind to ephrins pfam00812 are a large family of receptor tyrosine kinases. This family represents the amino terminal domain which binds the ephrin ligand.

CD-Length = 174 residues, 100.0% aligned

Score = 345 bits (886), Expect = 6e-96

```
Query:   33   QVVLLDTSTVMGELGWKTYPLNGWDAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWIS   92
              +V LLDT+T  GELGW TYP  GW+ ++ +DE+NRPI TYQVCNVMEPNQNNWLRTNWI
Sbjct:    1   EVTLLDTTTATGELGWLTYPPGGWEEVSGLDENNRPIRTYQVCNVMEPNQNNWLRTNWIP   60

                                      o  o  o       o     o   o
Query:   93   RDAAQKIYVEMKFTLRDCNSIPWVLGTCKETFTLYYIESDESHGTKFKPSQYIKIDTIAA   152
              R  AQ++YVE+KFT+RDCNS+P VLGTCKETF LYY ESDE  G  ++ +QY K+DTIAA
Sbjct:   61   RRGAQRVYVELKFTVRDCNSLPGVLGTCKETFNLYYYESDEDVGPAWRENQYTKVDTIAA   120

Query:  153   DESFTQMDLGDRILKLNTEIREVGPIERKGFYLAFQDIGACIALVSVRVFYKKC   206
              DESFTQ+DLGDR++KLNTE+R VGP+ +KGFYLAFQD+GAC+ALVSVRVFYKKC
Sbjct:  121   DESFTQVDLGDRVMKLNTEVRSVGPLSKKGFYLAFQDVGACMALVSVRVFYKKC   174   (SEQ
ID NO: 185)
```

Please replace Table 7E on pages 92-93 with the following:

Table 7E. Domain Analysis of NOV7

gnl|Pfam|pfam00083, sugar_tr, Sugar (and other) transporter.

CD-Length = 447 residues, 96.6% aligned
Score = 246 bits (629), Expect = 2e-66

```
Query:   21  FQVFKSFYNETYFERHATFM----DGKLMLLLWSCTVSMFPLGGLLGSLLVGLLVDSCGR   76
             V   F      F        +          +L    VS+F +G  +GSL   G  L D   GR
Sbjct:   16  TGVIGGFATLIDFLFFFGGLTSSGSCAESTVLSGLVVSIFFVGRPIGSLFAGKLGDRFGR   75

Query:   77  KGTLLINNIFAIIPAILMGVSKVAKAFELIVFSRVVLGVCAGISYSALPMYLGELAPKNL  136
             K +LLI  +  +I ++L G++   A  F L++  RV++G+   G +     +PMY+ E+APK L
Sbjct:   76  KKSLLIGLVLFVIGSLLSGLAPGA--FYLLIVGRVLVGLGVGGASVLVPMYISEIAPKAL  133

Query:  137  RGMVGTMTEVFVIVGVFLAQIFSLQAILGNPAGWPVLLALTGVPALLQLLTLPFFPESPR  196
             RG +G++ ++ +  +G+ +A I   L      N  GW +  L L  VPALL L+  L F  PESPR
Sbjct:  134  RGALGSLYQLGITIGILVAAIIGLGLNKTNNWGWRIPLGLQLVPALLLLIGLLFLPESPR  193

Query:  197  YSLIQKGDEATARPLRRLRGHTDMEAELEDMRAEARAERAEGHLSVLHLCALRSLRWQLL  256
             +  +++    E      L +LRG  D++ E+++ +AE   A  +         +     R +LL
Sbjct:  194  WLVLKGKLEEARAVLAKLRGVEDVDQEIQEEKAELEAGVSSEKAGLELF--RGRTRQRLL  251

Query:  257  SIIVLMAGQQLSGINAINYYADTIYTSAGVEAAHSQYVTVGSGVVNIVMTITSVVLVERL  316
             ++L   QQL+GINAI YY+ TI+ S G+  + +  VT+   GVVN V T   ++ LV+R
Sbjct:  252  MGVMLQIFQQLTGINAIFYYSPTIFKSVGMSDSVALLVTIIVGVVNFVATFVAIFLVDRF  311

Query:  317  GRRHLLLAGYGICGSACLVLTVSPPPQNRVPELSYLGIICVFAYIAGHSIGPSPVPSVVR  376
             GRR LLL G        L+L V+      P    + I+ +   +IA  ++G  P+P V+
Sbjct:  312  GRRPLLLLGAAGMAICFLILGVA-LLLLNKPGAGIVAIVFILLFIAFFALGWGPIPWVIL  370

Query:  377  TEIFLQSSRRAAFMVDGAVHWLTNFIIGFLFPSIQEAIG-AYSFIIFAGICLLTAIYIYV  435
             +E+F    R  A  + A +  +WL NFIIGFLFP I  AIG  Y F+ FAG+ +L  +++Y
Sbjct:  371  SELFPTGVRSKAMALATAANWLANFIIGFLFPYITGAIGGGYVFLFFAGLLVLFILFVYF  430

Query:  436  VIPETKGKTFVEINRIF    452
             +PETKG+T  EI+ +F
Sbjct:  431  FVPETKGRTLEEIDELF    447 (SEQ ID NO: 186)
```

Please replace Table 8E on page 101 with the following:

<table>
<tr><td colspan="3">Table 8E. Domain Analysis of NOV8</td></tr>
<tr><td colspan="3">gnl|Smart|smart00179, EGF_CA, Calcium-binding EGF-like domain</td></tr>
<tr><td colspan="3">CD-Length = 41 residues, 80.5% aligned</td></tr>
<tr><td colspan="3">Score = 52.8 bits (125), Expect = 7e-08</td></tr>
<tr><td>Query: 125</td><td>DIDECEVSGLCRHGGRCVNTHGSFECY-CMDGY</td><td>156</td></tr>
<tr><td></td><td>DIDEC   C++GG CVNT GS+ C   C   GY</td><td></td></tr>
<tr><td>Sbjct: 1</td><td>DIDECASGNPCQNGGTCVNTVGSYRCEECPPGY</td><td>33 (SEQ ID NO:</td></tr>
<tr><td>187)</td><td></td><td></td></tr>
</table>

Please replace Table 9E on page 109 with the following:

<table>
<tr><td colspan="3">Table 9E. Domain Analysis of NOV9</td></tr>
<tr><td colspan="3">gnl|Smart|smart00179, EGF_CA, Calcium-binding EGF-like domain</td></tr>
<tr><td colspan="3">CD-Length = 41 residues, 80.5% aligned</td></tr>
<tr><td colspan="3">Score = 52.8 bits (125), Expect = 7e-08</td></tr>
<tr><td>Query: 125</td><td>DIDECEVSGLCRHGGRCVNTHGSFECY-CMDGY</td><td>156</td></tr>
<tr><td></td><td>DIDEC   C++GG CVNT GS+ C   C   GY</td><td></td></tr>
<tr><td>Sbjct: 1</td><td>DIDECASGNPCQNGGTCVNTVGSYRCEECPPGY</td><td>33 (SEQ ID NO:</td></tr>
<tr><td>188)</td><td></td><td></td></tr>
</table>

Please replace Table 10E on page 116 with the following:

```
                    Table 10G Domain Analysis of NOV10

              gnl|Smart|smart00409, IG, Immunoglobulin

                    CD-Length = 86 residues, 89.5% aligned
                    Score = 37.0 bits (84), Expect = 0.001

Query:  27  SNVTLECNFDTGSHVNLGAITVSLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVR  86
            +VTL C             TV+ K            R ++       G ++  I  V
Sbjct:  10  ESVTLSCEASGNPPP-----TVTWYKQGGKLLAESGRFSVSRSG---GNSTLTISNVTPE  61

Query:  87  DEGQYQCIIIYGVAWDYKYLTLKVK  111
            D G Y C              TL V
Sbjct:  62  DSGTYTCAATNSSGSASSGTTLTVL  86  (SEQ ID NO: 189)
```

Please replace Table 11E on page 123 with the following:

```
                    Table 11E. Domain Analysis of NOV11

              gnl|Smart|smart00406, IGv, Immunoglobulin V-Type

                    CD-Length = 80 residues, 96.2% aligned
                    Score = 34.7 bits (78), Expect = 0.008

Query:  52   VELQCQLFPNISAEDMELRWYRCQPSLAVHMHERGMDMDGEQKWQYRGRTTFMSDHVARG  111
             V L C+      +     + W R  P  +              +  Y+GR T   D+ ++
Sbjct:  2    VTLSCKASGF-TFSSYYVSWVRQPPGKGLEWLGYIGSDVSYSEASYKGRVTISKDN-SKN  59

Query:  112  KAMVRSHRVTTFDNRTYCC  130
               +     D  TY C
Sbjct:  60   DVSLTISNLRVEDTGTYYC  78  (SEQ ID NO: 190)
```

Please insert the sequence listing pages 1-198 at the end of the specification.

REMARKS

In response to the March 27, 2002 Notice to File Missing Parts of Nonprovisional

Application, Applicants submit herewith a computer readable form (CFR) copy of the "Sequence

Listing"; a paper copy of the "Sequence Listing"; and a statement that the content of the paper

and computer readable copies are the same and include no new matter, in